

SbHSP60-1	89	38	9	35	24	5	17	100	3	0	3	6	4	20	2	5	6	1
SbHSP60-2	48	26	8	27	18	1	9	41	2	4	3	5	0	5	5	4	3	0
SbHSP60-3	154	56	16	66	29	8	22	145	4	3	8	17	10	41	7	7	5	5
SbHSP60-4	70	48	17	50	9	4	13	85	3	4	5	4	8	19	13	9	9	4
SbHSP60-5	27	23	5	15	7	0	5	31	2	2	3	5	4	10	2	2	1	0
SbHSP60-6	60	32	12	35	17	1	13	64	2	2	5	1	5	17	4	5	5	2
SbHSP60-7	34	17	4	17	7	1	7	33	1	1	0	3	2	7	1	2	1	0
SbHSP60-8	37	30	6	28	3	1	8	44	1	2	2	2	5	14	6	3	1	2
SbHSP60-9	80	45	10	41	12	4	16	90	4	2	5	6	7	17	7	6	5	7
SbHSP60-10	116	41	14	46	22	3	21	105	4	3	6	8	12	23	6	11	6	6
SbHSP60-11	14	21	3	14	5	0	3	18	0	1	2	0	1	0	1	1	1	2
SbHSP60-12	38	30	2	30	10	5	10	39	1	0	4	5	3	11	1	1	0	2
SbHSP60-13	43	23	0	27	8	4	12	32	0	0	4	3	4	8	2	3	2	4
SbHSP60-14	119	43	11	41	40	2	16	98	2	4	8	9	15	28	5	4	6	4
SbHSP60-15	20	21	10	15	13	0	3	31	2	2	1	4	1	5	0	1	0	0
SbHSP60-16	105	45	6	50	14	2	23	69	0	1	5	10	13	40	1	1	2	1
SbHSP60-17	20	15	3	11	3	0	5	22	0	0	3	3	1	4	2	3	0	0
SbHSP60-18	104	50	18	55	27	3	18	100	2	4	7	9	10	21	2	3	3	3
SbHSP60-19	13	2	1	9	0	0	3	13	0	1	1	0	1	4	0	0	0	1
SbHSP60-20	115	38	13	48	30	4	22	101	1	6	4	9	7	27	4	2	5	3
SbHSP60-21	139	51	20	56	35	5	19	122	0	5	5	16	10	33	11	13	7	4
SbHSP60-22	106	47	17	50	19	6	20	99	0	5	10	9	9	20	15	16	13	5
SbHSP60-23	147	36	16	58	18	6	26	120	2	2	9	8	12	32	8	10	5	2
SbHSP60-24	80	35	21	36	13	0	21	75	2	2	4	2	6	25	3	5	3	3
SbHSP60-25	59	45	8	40	17	2	15	71	2	0	5	5	4	9	3	2	3	2
SbHSP60-26	54	36	7	33	14	4	15	62	2	2	6	3	4	14	0	0	1	0
SbHSP60-27	28	28	10	22	9	2	6	47	2	2	3	3	3	7	1	0	1	0
SbHSP60-28	172	59	28	67	31	13	36	169	4	6	12	14	15	46	17	11	7	2
SbHSP60-29	17	19	5	17	3	0	2	23	1	1	2	2	2	3	1	1	0	2
SbHSP60-30	69	42	16	39	12	5	18	65	4	3	7	5	7	17	6	8	7	3
SbHSP10																		
SbHSP10-1	9	1	1	4	2	0	2	4	0	1	1	0	0	3	1	0	0	0
SbHSP10-2	21	2	2	13	0	0	4	13	0	0	0	2	2	5	0	0	0	0
SbHSP10-3	5	5	0	5	1	0	1	5	0	0	1	0	0	0	1	1	0	0

SbHSP10-4	137	67	13	74	26	5	30	135	4	2	14	15	11	19	14	17	10	4
SbHSP10-5	29	20	2	16	3	3	8	30	1	0	2	2	5	6	2	2	2	3
SbHSP10-6	91	60	9	58	12	3	21	96	1	0	5	4	18	25	13	8	6	9

Table S3. *Cis*-acting elements present in the promoter regions of *Sorghum* HSP60 family

	DRE	DPBF	MYB	MYC	HSE	LTRE	GT1GM	ACGTATERD1	PIBS	BHDIOS	RYREPEAT	CBHV	CAREOSREPI	L-Box	ARR1	ABRE	GARE	SK ₂	Pollen	WBOXAINPR1	WBOXHVISI	WBOXNTERF3	WRKY1	TKST1	MARTBOX	SEEMOTIFGM	GTGANTG10	GTICONSENSUS	GATABOX	ANAEROL	CACTFPPCAL	SORLI2AT	SITEIATCYTC	DOF	SURECORE	ERELEF4	RHERPATEXPAT7	ARFAT	CPBCSPOR	Me-Id
SbHSP60-1	3	3	13	6	3	1	5	3	0	4	1	3	1	4	17	2	0	3	8	2	4	6	11	4	6	6	11	24	10	6	17	7	2	36	3	2	1	0	2	0
SbHSP60-2	2	1	8	9	2	5	0	8	0	2	0	3	0	0	4	20	0	0	1	0	0	3	10	0	0	0	12	1	3	4	12	28	11	3	1	0	4	0	0	2
SbHSP60-3	0	3	8	3	3	1	5	8	1	5	3	0	0	3	13	7	1	2	7	3	2	3	10	4	3	4	9	14	6	4	22	10	4	22	3	0	3	0	1	0
SbHSP60-4	2	6	14	7	2	5	1	5	0	4	1	5	1	4	20	7	0	1	8	4	1	3	13	5	0	8	17	17	9	7	49	6	2	19	4	0	4	2	1	0
SbHSP60-5	1	0	8	6	5	3	9	0	1	2	3	2	0	3	28	0	0	1	11	2	2	5	9	6	3	4	12	27	12	1	27	7	1	34	0	1	1	1	1	2
SbHSP60-6	0	0	22	10	7	4	7	3	0	7	0	0	1	4	17	7	2	4	16	4	4	6	18	3	1	1	10	18	14	6	38	6	3	23	0	0	2	0	0	2
SbHSP60-7	1	2	15	5	6	2	4	3	1	2	5	2	0	9	21	4	2	1	11	4	3	6	10	3	0	8	4	15	23	5	35	2	1	25	1	1	4	0	4	0
SbHSP60	2	7	10	8	1	1	4	2	0	5	4	3	1	11	11	2	0	2	5	7	6	15	24	2	3	19	8	16	6	35	2	2	20	5	0	0	2	2	0	

- 8	2	4	1	7	2	1	1	5	0	8	0	3	2	1	2	7	0	3	4	6	4	1	2	1	0	5	1	6	1	0	1	8	4	3	1	2	0	0	2	0	3	3	
S b H S P 6 0 - 9	2	2	1	5	3	1	2	4	1	5	0	2	1	3	1	4	0	4	6	3	4	8	1	1	2	3	1	1	1	2	5	2	5	2	1	7	3	0	1	1	4	2	
S b H S P 6 0 - 1 0	0	1	1	9	6	0	3	1	0	7	2	0	0	7	2	1	0	1	9	1	3	8	1	5	1	7	1	1	1	2	2	4	4	1	1	4	0	1	1	0	2	1	
S b H S P 6 0 - 1 1	6	7	1	1	9	8	2	7	0	1	1	7	1	1	1	2	0	0	1	3	4	8	1	2	1	2	1	9	6	2	2	2	3	8	1	2	0	7	0	3	0		
S b H S P 6 0 - 1 2	2	3	1	4	8	2	1	2	3	1	0	7	2	6	6	1	1	9	2	3	6	9	5	0	3	1	0	2	1	3	3	1	1	4	2	2	3	1	0	2	1	0	
S b H S P 6 0 - 1 3	3	5	1	1	5	3	3	8	1	1	0	2	3	1	1	1	5	4	4	3	9	6	5	1	2	6	3	0	2	1	1	1	2	4	2	5	4	4	1	3	0	0	0
S b H S P 6 0 - 1 4	1	2	2	1	1	3	6	3	1	3	8	2	1	3	1	3	5	3	4	4	4	9	1	8	3	8	1	1	1	1	2	4	5	2	9	3	0	1	2	4	0		
S b H S P 6 0 - 1 5	3	2	1	1	1	3	4	4	0	5	1	3	0	3	2	8	2	2	1	3	3	5	1	4	0	2	2	1	1	9	2	7	2	1	5	1	4	3	1	1			
S b H S P 6 0 - 1 6	4	3	1	9	7	5	6	6	0	6	0	4	0	3	1	8	1	0	1	5	1	3	1	5	1	2	9	1	1	5	2	3	1	2	2	2	1	4	0	0	0		
S b H S P 6 0 - 1 7	2	2	2	7	8	5	1	2	1	3	8	1	3	3	2	3	3	2	1	5	0	5	1	7	2	1	8	3	1	8	3	2	2	3	4	4	0	2	0	0	2		

SbHSP60-28	1	6	1	1	4	0	1	5	0	6	3	0	1	7	1	1	0	1	9	2	3	5	1	2	0	2	2	1	1	3	6	3	3	6	0	1	3	0	1	1	0	1
SbHSP60-29	0	2	8	8	3	1	4	2	0	4	6	1	0	5	3	0	1	1	1	6	3	3	5	1	3	1	1	1	1	5	8	8	3	5	2	1	3	3	0	1	0	2
SbHSP60-30	2	3	1	1	1	2	0	4	0	5	3	1	3	4	1	5	0	1	7	5	6	1	1	1	1	1	2	1	4	1	4	3	7	4	3	1	3	0	3	0	0	0
HSP-10																																										
SbHSP10-1	0	4	1	1	4	1	2	8	1	4	1	1	1	0	1	8	0	2	8	2	3	6	1	2	0	5	1	6	1	6	3	7	2	5	1	4	2	0	0			
SbHSP10-2	5	2	1	1	4	2	5	3	1	7	1	4	0	7	1	6	1	5	5	2	3	6	1	3	0	2	1	9	1	4	2	8	2	1	1	1	0	1	1			
SbHSP10-3	0	1	1	9	5	0	1	6	1	4	0	1	1	4	1	7	1	3	7	3	3	5	1	3	0	2	1	1	9	2	2	1	4	9	0	0	3	0	4			
SbHSP10-4	0	2	2	1	5	0	6	5	0	4	2	0	4	1	1	6	2	1	1	6	6	1	1	8	2	7	1	2	2	2	1	3	2	2	7	3	0	1	0	1		
SbHSP10-5	0	1	1	1	5	1	3	3	1	8	1	0	0	1	9	0	0	2	6	3	1	2	1	4	0	6	1	1	2	1	3	3	0	3	1	1	3	0	0			
SbHSP10-6	4	3	9	4	1	4	1	4	0	4	1	0	4	1	0	5	7	0	2	2	1	4	4	1	2	0	4	1	4	3	4	2	1	3	2	7	5	0	5	2	0	

Table. S5 Non-synonymous to synonymous substitution rates (dN/dS) of SbHSP60 paralogs

SbHSP60 Gene 1	Chr	SbHSP60 Gene 2	Chr	No. of non-synonymous sites (N)	No. of synonymous sites (S)	Non-synonymous substitution rate (d_N)	Synonymous substitution rate (d_S)	d_N/d_S	Mya
SbHSP60-01	1	SbHSP60-25	9	2811.4	680.6	7.7152	0.0779	99.0000	5.99
SbHSP60-03	1	SbHSP60-14	7	4551.8	881.2	6.4569	0.0652	99.0000	5.01
SbHSP60-04	1	SbHSP60-16	4	4313.6	1017.4	9.3073	0.0940	99.0000	7.23
SbHSP60-05	1	SbHSP60-30	u	1691.6	372.4	6.4812	0.0655	99.0000	5.03
SbHSP60-06	1	SbHSP60-18	5	2939.3	600.7	5.9845	0.0604	99.0000	4.64
SbHSP60-08	2	SbHSP60-29	10	1304.8	354.2	1.5741	1.3860	1.1357	10.66
SbHSP60-10	2	SbHSP60-22	7	3214.8	640.2	6.5080	0.0657	99.0000	5.05
SbHSP60-12	3	SbHSP60-13	3	1884.1	440.9	6.5614	0.0663	99.0000	5.1
SbHSP60-19	5	SbHSP60-26	9	353.3	93.7	6.0015	0.0606	99.0000	4.66
SbHSP60-20	6	SbHSP60-21	7	3964.3	718.7	7.2582	0.0733	99.0000	5.63
SbHSP10-1	1	SbHSP10-06	10	303.1	98.9	17.1868	0.1736	99.0000	13.35
SbHSP10-2	1	SbHSP10-3	2	395.0	88.0	2.7957	6.1591	0.4539	47.37

($d_N/d_S > 1$ = Positive or Darwinian Selection (Driving Change); $d_N/d_S < 1$ = Purifying or Stabilizing Selection (Acting against change); $d_N/d_S = 1$ Neutral Selection)

Table S6. Non-synonymous to synonymous substitutions of HSP60 orthologs of *Sorghum*, *Oryza* and *Arabidopsis*

Sb60 Gene	Chr	Ortholog	Chr	No. non Synonymous sites (N)	No. Synonymous sites (S)	Non Synonymous substitution rate (d_N)	Synonymous substitution rate (d_S)	d_N / d_S	Mya
Sb02g024300	2	Os09g23740	12	3051.2	803.8	3.2149	2.4773	1.2978	19.05
Sb07g020930	7	Os08g33200	8	3719.7	939.3	3.4622	2.9442	1.1759	22.64
Sb10g009370	10	Os06g14750	6	3621.3	1205.7	7.8677	1.9410	4.0534	14.93
Sb07g022110	7	Os08g34950	8	4518.3	914.7	5.8990	0.0596	99.0000	4.58
Sb03g041400	3	Os12g13440	12	4155.8	701.2	6.4122	0.0648	99.0000	4.98
Sb06g034080	6	Os04g59540	4	3485.0	637.0	8.3735	0.0846	99.0000	6.50
Sb01g028650	1	Os10g41710	10	295.3	106.7	12.3425	14.8203	0.8328	114.0
Sb10g006450	10	Os06g09679	6	648.5	182.5	16.6103	0.1678	99.0000	12.90
Sb04g035040	4	Os02g54060	2	585.1	179.9	1.5289	2.2074	0.6926	16.98
Sb02g025700	2	Os09g26730	9	570.7	164.3	16.6950	0.1686	99.0000	12.96
Sb02g011260	2	Os09g38980	9	587.6	147.4	6.0110	0.0607	99.0000	78.91
Sb01g000380	1	Os03g64210	3	1359.3	392.7	10.7306	0.1084	99.0000	8.33
Sb09g014430	9	Os12g17910	12	1369.0	365.0	7.1946	0.0727	99.0000	5.59
Sb04g000370	4	Os02g01280	2	1401.8	326.2	15.9874	0.1615	99.0000	12.42
Sb01g041170	1	Os04g0443900	4	1373.2	390.8	14.4551	7.8874	1.8327	60.67
Sb09g026970	9	Os05g0540300	5	1395.9	347.1	3.9401	0.1431	27.5367	11.0
Sb01g043220	1	Os06g34690	6	1251.0	423.0	4.8892	2.4069	2.0314	18.51
Sb04g004030	4	Os06g47320	6	1297.8	370.2	0.3544	0.3348	1.0558	25.75
Sb05g022470	5	Os11g36950	3	344.5	78.5	8.9983	0.0909	99.0000	6.99
Sb02g043440	2	Os05g0147400	5	1310.6	294.4	8.4378	0.0852	99.0000	6.55

Sb01g034530	1	Os03g25050	3	302.8	105.2	11.2831	10.3233	1.0930	79.41
Sb01g028650	1	Os10g41710	10	310.5	91.5	7.8735	0.0795	99.0000	6.11
Sb07g000590	7	Os08g01390	8	4089.6	740.4	6.7712	0.0684	99.0000	5.26

($d_N/d_S > 1$ = Positive or Darwinian Selection (Driving Change); $d_N/d_S < 1$ = Purifying or Stabilizing Selection (Acting against change); $d_N/d_S = 1$ Neutral Selection)

Table S7. qRT-PCR expression levels of SbHSP60s

Tissue / Stress	Name of the gene and their expression							
	SbHSP60-1	SbHSP60-2	SbHSP60-3	SbHSP60-6	SbHSP60-9	SbHSP60-24	SbHSP10-2	SbHSP10-5
R	0.32	0.01	0.15	0.10	-0.26	0.09	0.10	-0.60
S	-0.40	-0.46	-0.79	-0.72	-0.99	-0.45	-0.32	-0.74
L	0.08	0.45	0.65	0.62	1.25	0.35	0.22	1.35
DR	2.38943	2.229417	4.046477	0.8625422	5.924390	1.289370	5.96559	3.96320
SR	2.92817	1.558329	14.32040	47.176614	10.05610	0.624165	1.53687	0.59460
HR	6.68070	2.013911	29.24260	0.4263174	0.562529	1.547564	5.81589	0.04450
CR	0.11907	0.141610	0.336808	9.4479412	9.986644	18.63573	0.14161	0.01991
DS	0.25173	0.130308	0.517632	4.1698630	17.63048	3.249009	0.05041	0.05440
SS	7.74536	2.815387	2.060984	2.1189261	2.874544	2.663518	11.6586	0.03025
HS	0.18258	0.244289	0.307075	23.862390	18.33675	12.35194	0.06149	0.24092
CS	0.43931	0.374576	1.397969	1.5619338	224.9301	82.32925	0.64319	30.5549
DL	12.6699	0.656712	3.792984	1.1276609	3.348078	71.67178	0.96817	0.01154
SL	1.32256	1.594753	19.07132	1.1674278	16.03701	0.529731	0.58777	0.42435
HL	0.18772	0.103425	3.131093	0.0527994	1.236846	0.010284	0.49197	0.71532
CL	4.73489	1.208597	23.97291	0.1177120	5.910717	0.187288	100.659	3.79298

(R; Root, S: Stem, L: Leaf, D: Drought, S: Salt, H: Heat, C: Cold)



Fig S2. MEME identified motif sequences of *Sorghum* Hsp10 proteins

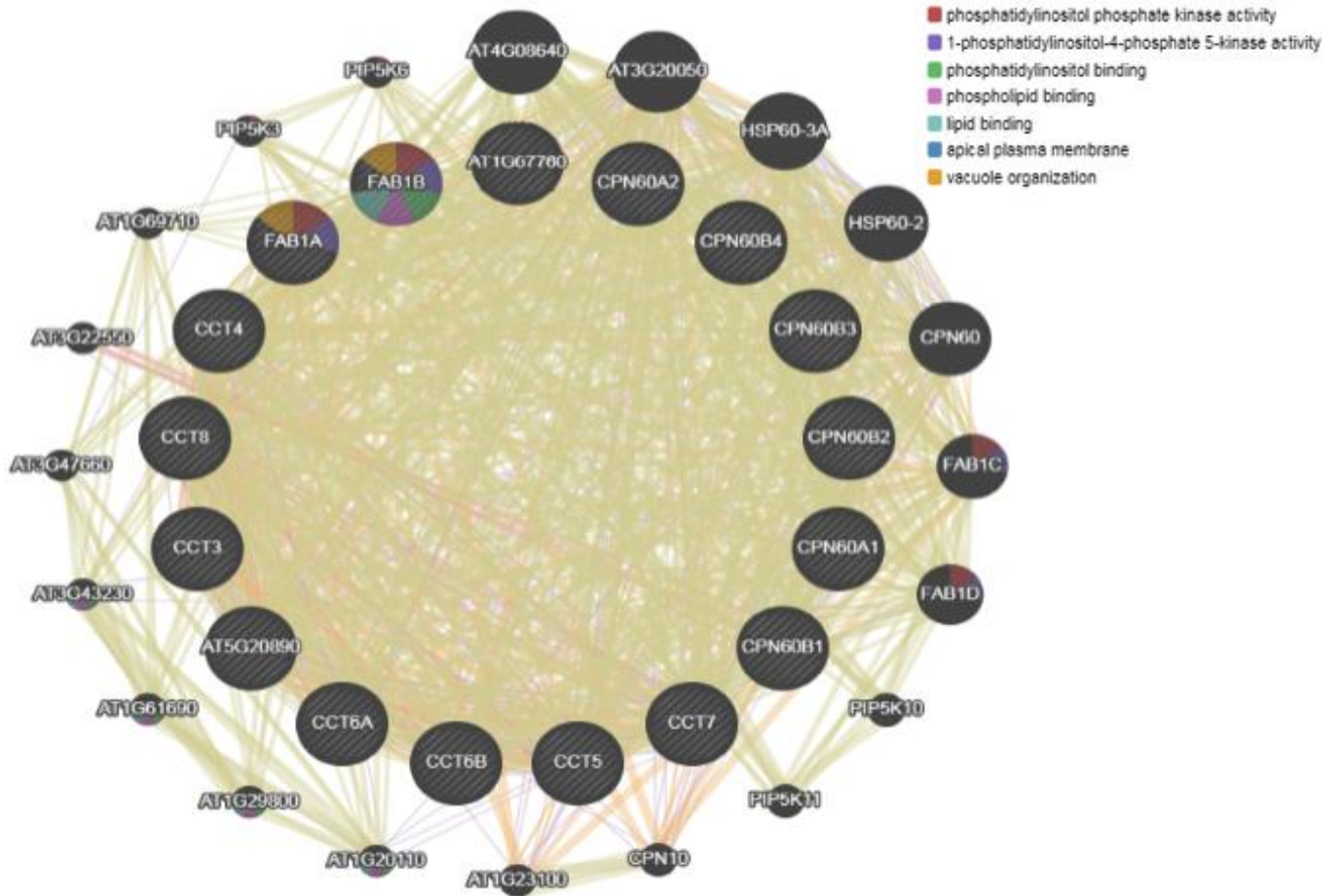


Fig S3. Gene-gene interaction and GO annotation analysis of SbHSP60s

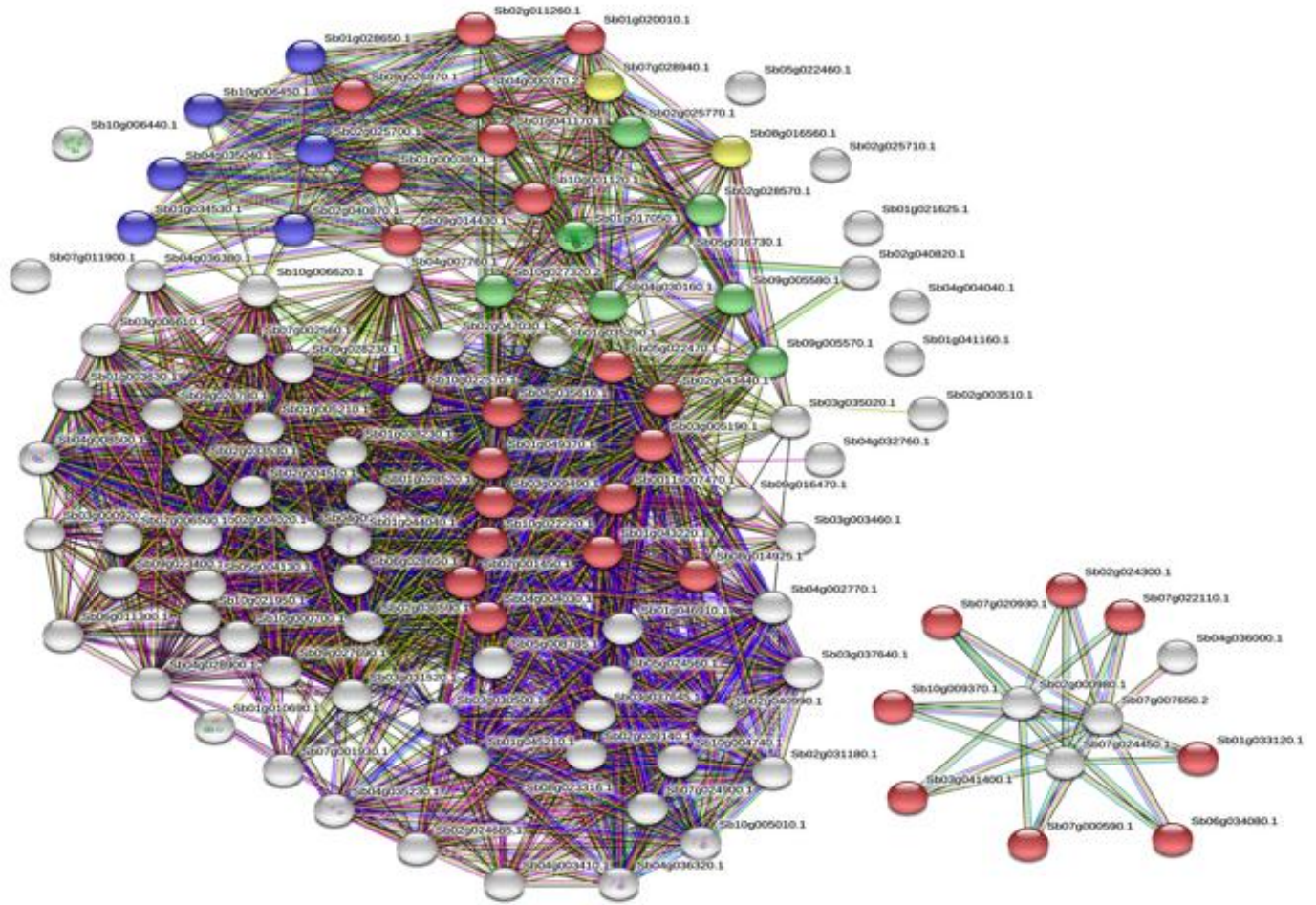


Fig S4. STRING identified protein – protein interactions of Hsp60 in *Sorghum*

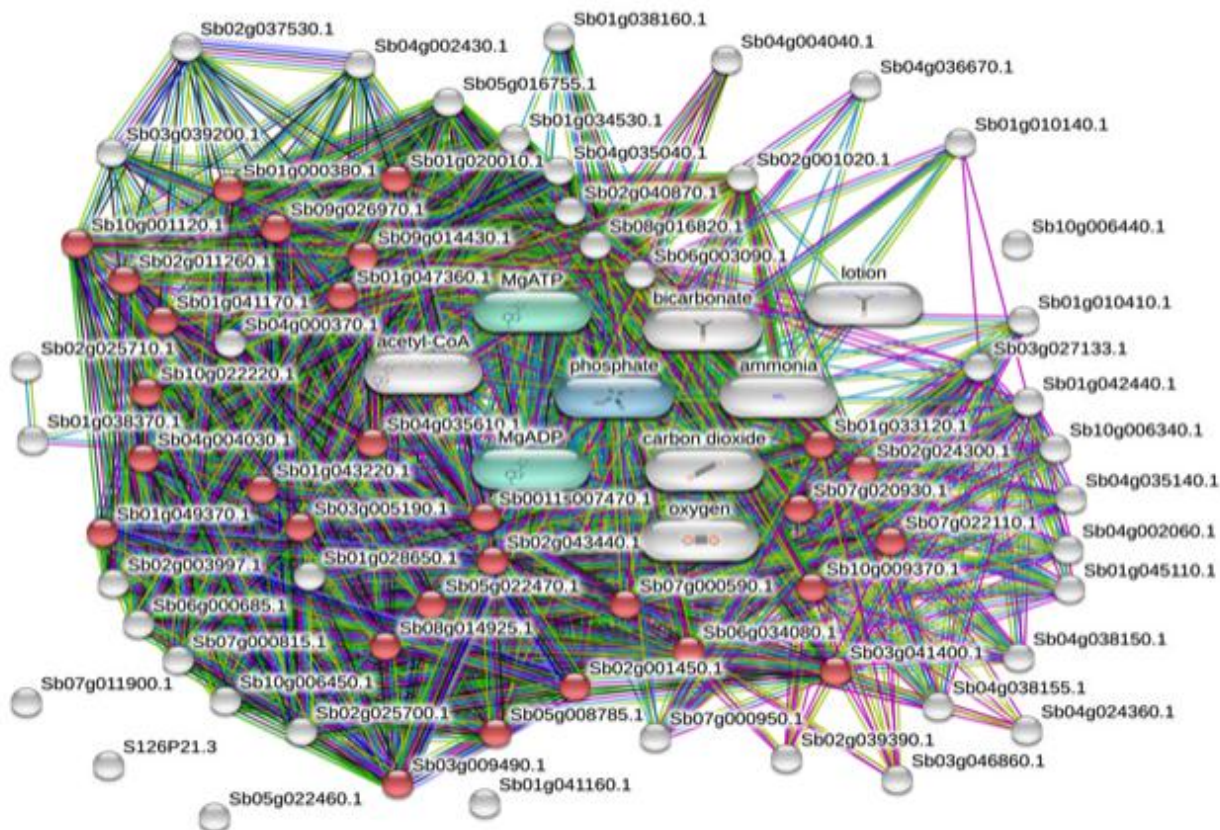


Fig S5. Protein – chemical interaction network of of SbHsp60s

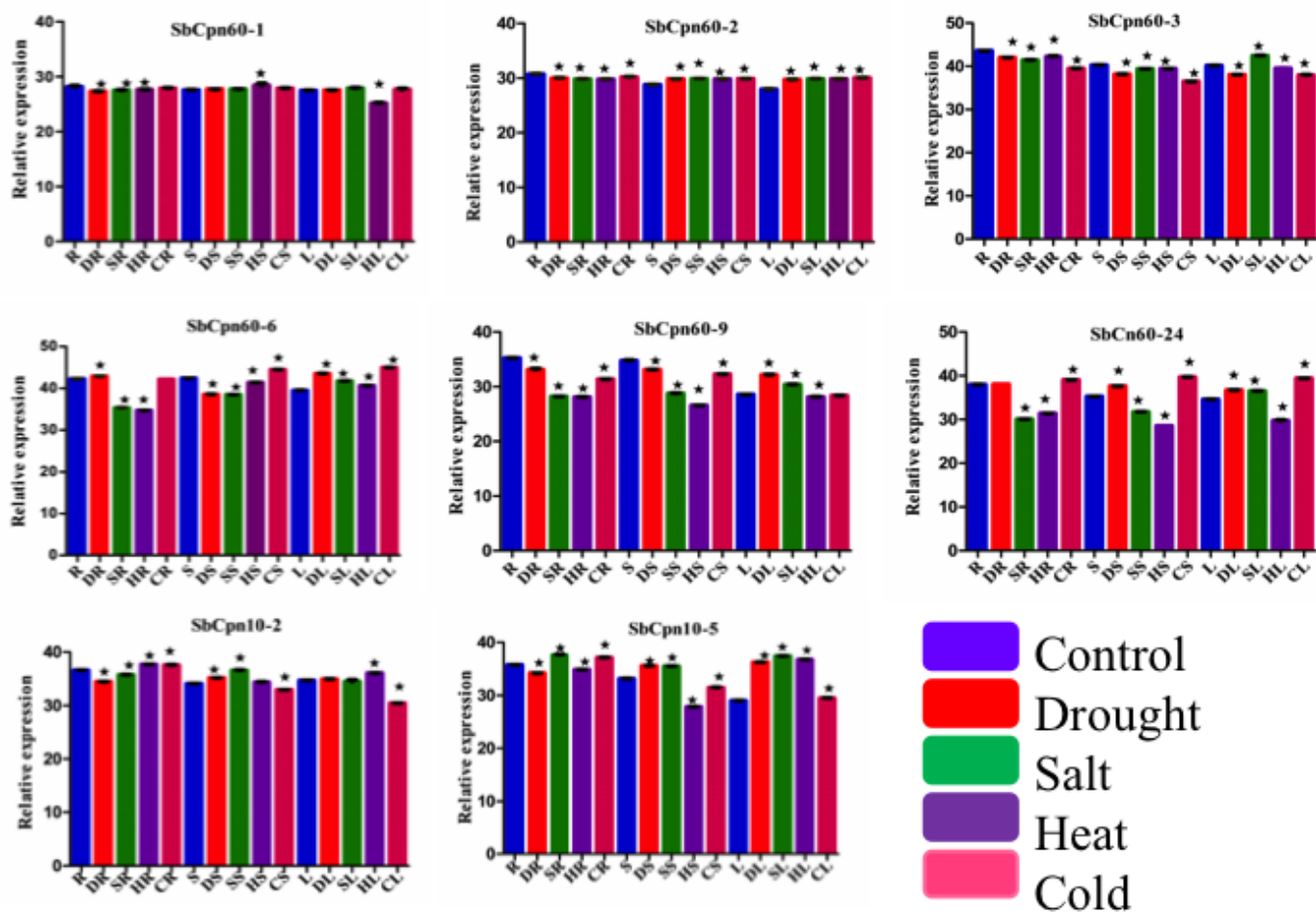


Fig. S6 The qRT-PCR relative expression values of selected *SbHsp60* genes in root, stem, and leaves under drought, salt, heat and cold stress (DR: Drought root, DS: Drought stem, DL: Drought Leaf, SR: Salt root, SS: Salt stem, SL: Salt leaf, HR: Heat root, HS: Heat stem, HL: Heat leaf, CR: Cold root, CS: Cold stem, CL: Cold leaf). Each values represents mean \pm SD of three replicates. * indicate significant differences calculated by t-test ($P \leq 0.05$).